



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 31542986 ref NP_060095.2 	intelectin; endothelial lectin...		743	0.0	L
gi 7019846 dbj BAA90893.1 	unnamed protein product [Homo sa...		743	0.0	L
gi 37724005 gb AAO17800.1 	intelectin [Homo sapiens]		740	0.0	L
gi 18254480 ref NP_543154.1 	intelectin 2; endothelial lect...		534	e-150	L
gi 6754388 ref NP_034714.1 	intelectin [Mus musculus] >gi 7...		528	e-148	L
gi 28932914 gb AAO60215.1 	intelectin 2 [Mus musculus]		491	e-137	
gi 45360437 ref NP_988929.1 	hypothetical protein MGC76330 ...		360	5e-98	L
gi 20502359 dbj BAB91359.1 	35 kDa serum lectin [Xenopus la...		353	5e-96	L
gi 28971732 dbj BAC65329.1 	embryonic epidermal lectin [Xen...		352	1e-95	L
gi 20502361 dbj BAB91360.1 	lectin type 2 [Xenopus laevis]		338	2e-91	L
gi 2632076 emb CAA57946.1 	cortical granule lectin [Xenopus...		324	3e-87	L
gi 1841845 gb AAB47537.1 	lectin [Xenopus laevis]		322	1e-86	L
gi 45360965 ref NP_988850.1 	egg cortical granule lectin [X...		301	2e-80	L
gi 1079283 pir S49589	cortical granule lectin - African cl...		252	2e-65	
gi 13094239 dbj BAB32787.1 	serum lectin [Lethenteron japon...		224	5e-57	
gi 11095793 gb AAG30025.1 	putative interlectin [Oncorhynch...		107	6e-22	
gi 42524003 ref NP_969383.1 	hypothetical protein predicted...		49	2e-04	

gi 42524002 ref NP_969382.1 	hypothetical protein predicted...	<u>47</u>	8e-04	
gi 47229454 emb CAF99442.1 	unnamed protein product [Tetrao...	<u>40</u>	0.12	
gi 6753006 ref NP_033771.1 	angiopoietin 4; angiopoietin 3 ...	<u>40</u>	0.12	L
gi 47228399 emb CAG05219.1 	unnamed protein product [Tetrao...	<u>38</u>	0.39	
gi 553348 gb AAA52703.1 	hexabrachion	<u>38</u>	0.52	L
gi 184484 gb AAA88083.1 	hexabrachion	<u>38</u>	0.52	L
gi 37227 emb CAA39628.1 	tenascin [Homo sapiens]	<u>38</u>	0.52	L
gi 4504549 ref NP_002151.1 	tenascin C (hexabrachion); Hexa...	<u>38</u>	0.52	L
gi 34858971 ref XP_215890.2 	similar to angiopoietin 3 [Rat...	<u>38</u>	0.52	L
gi 30316326 sp P02678_2	[Segment 2 of 2] Fibrinogen beta c...	<u>38</u>	0.70	
gi 7441528 pir A25052	fibrinogen beta chain - sea lamprey ...	<u>38</u>	0.70	
gi 23200381 pdb 1LWU B	Chain B, Crystal Structure Of Fragme...	<u>38</u>	0.70	S
gi 18858273 ref NP_571889.1 	angiopoietin 2 [Danio rerio] >...	<u>37</u>	1.3	L
gi 14349157 dbj BAB60705.1 	ficolin 2 [Halocynthia roretzi]	<u>36</u>	1.7	
gi 27668503 ref XP_220264.1 	similar to M83 protein [Rattus...	<u>36</u>	2.3	L
gi 47086505 ref NP_997939.1 	Unknown (protein for MGC:77116...	<u>36</u>	2.3	L
gi 13543090 gb AAH05722.1 	Tmem8 protein [Mus musculus]	<u>36</u>	2.3	L
gi 11140833 ref NP_068565.1 	transmembrane protein 8 (five ...	<u>36</u>	2.3	L
gi 91806 pir JQ1322	tenascin precursor - mouse >gi 220610 ...	<u>35</u>	4.1	L
gi 558867 gb AAA50761.1 	tenascin	<u>35</u>	4.1	
gi 29290612 emb CAD83048.1 	bN144L11.1.2 (tenascin C, varia...	<u>35</u>	4.1	
gi 7106435 ref NP_035737.1 	tenascin C [Mus musculus] >gi 5...	<u>35</u>	4.1	L
gi 47523544 ref NP_999395.1 	tenascin C; hexabrachion [Sus ...	<u>35</u>	5.5	L
gi 10441960 gb AAG17257.1 	unknown [Homo sapiens]	<u>35</u>	5.5	L
gi 8570647 gb AAF76526.1 	angiopoietin-2 isoform-1 [Homo sa...	<u>35</u>	5.5	L
gi 7768835 dbj BAA95590.1 	Angiopoietin-2 [Homo sapiens]	<u>35</u>	5.5	L
gi 22001408 gb AAM88421.1 	OMFREP [Ornithodoros moubata]	<u>35</u>	5.5	
gi 4557315 ref NP_001138.1 	angiopoietin 2; Ang2 [Homo sapi...	<u>35</u>	5.5	L
gi 21313152 ref NP_083844.1 	microfibrillar-associated prot...	<u>34</u>	7.4	L
gi 12643645 sp O77802 AGP2 BOVIN	Angiopoietin-2 (ANG-2) >gi...	<u>34</u>	7.4	L
gi 47212658 emb CAF89485.1 	unnamed protein product [Tetrao...	<u>34</u>	7.4	
gi 35902868 ref NP_919364.1 	tenascin R (restrictin, janusi...	<u>34</u>	7.4	L
gi 48833154 ref ZP_00290177.1 	COG1357: Uncharacterized low...	<u>34</u>	7.4	
gi 27672001 ref XP_213313.1 	similar to RIKEN cDNA 1110007F...	<u>34</u>	7.4	L
gi 45199149 ref NP_986178.1 	AFR631Cp [Eremothecium gossypi...	<u>34</u>	9.9	
gi 26343315 dbj BAC35314.1 	unnamed protein product [Mus mu...	<u>34</u>	9.9	L
gi 10120284 emb CAC08176.1 	angiopoietin-2C [Gallus gallus]	<u>34</u>	9.9	
gi 10120282 emb CAC08175.1 	angiopoietin-2B [Gallus gallus]	<u>34</u>	9.9	L
gi 10120280 emb CAC08174.1 	angiopoietin-2A [Gallus gallus]	<u>34</u>	9.9	
gi 1589549 prf 2211329A	tenascin R	<u>33</u>	13	
gi 47523224 ref NP_998973.1 	angiopoietin 2 [Sus scrofa] >g...	<u>33</u>	13	L
gi 29789028 ref NP_071707.1 	tenascin R [Mus musculus] >gi ...	<u>33</u>	13	L
gi 45382035 ref NP_990787.1 	200 kd tenascin [Gallus gallus...	<u>33</u>	13	L
gi 104643 pir A32230	tenascin precursor - chicken >gi 2117...	<u>33</u>	13	L
gi 86243 pir A31930	cytotactin - chicken (fragments)	<u>33</u>	13	
gi 5730098 ref NP_003276.2 	tenascin R (restrictin, janusin...	<u>33</u>	13	L
gi 212748 gb AAA49085.1 	190 kd tenascin precursor	<u>33</u>	13	L
gi 211724 gb AAA48749.1 	cytotactin	<u>33</u>	13	
gi 1065718 emb CAA61489.1 	tenascin-C [Danio rerio]	<u>33</u>	13	L

gi 6981668 ref NP_037177.1	tenascin R; Tenascin-R (Restric...	33	13	L
gi 45384054 ref NP_990607.1	restrictin [Gallus gallus] >gi...	33	13	L
gi 212747 gb AAA49084.1	200 kd tenascin precursor	33	13	L
gi 1617316 emb CAA66709.1	tenascin-R [Homo sapiens]	33	13	L
gi 40018582 ref NP_954538.1	Unknown (protein for MGC:72631...	33	13	L
gi 47834361 gb AAT38877.1	angiopoietin 2 [Sus scrofa]	33	18	
gi 23822263 sp Q9HCN3 TME8_HUMAN	Transmembrane protein 8 pr...	33	18	L
gi 10437082 dbj BAB14975.1	unnamed protein product [Homo s...	33	18	L
gi 13751640 emb CAC37286.1	C367G8.2 (novel protein) [Homo ...	33	18	
gi 10864069 ref NP_067082.1	transmembrane protein 8 (five ...	33	18	L
gi 13279098 gb AAH04276.1	Unknown (protein for IMAGE:36154...	33	18	L
gi 13474653 ref NP_106222.1	unknown protein [Mesorhizobium...	33	18	
gi 8569622 pdb 1EI3 B	Chain B, Crystal Structure Of Native ...	33	18	S
gi 45383970 ref NP_990520.1	tenascin Y variant [Gallus gal...	33	18	L
gi 399491 sp Q02020 FIBB_CHICK	Fibrinogen beta chain precur...	33	18	L
gi 14336694 gb AAK61227.1	M83 [Homo sapiens]	33	18	
gi 14349159 dbj BAB60706.1	ficolin 3 [Halocynthia roretzi]	32	24	
gi 19483942 gb AAH23373.1	Similar to angiopoietin-like fac...	32	24	
gi 47210568 emb CAF94390.1	unnamed protein product [Tetrao...	32	24	
gi 14349155 dbj BAB60704.1	ficolin 1 [Halocynthia roretzi]	32	24	
gi 47217428 emb CAG00788.1	unnamed protein product [Tetrao...	32	24	
gi 10863949 ref NP_066969.1	angiopoietin-like factor [Homo...	32	24	L
gi 31200947 ref XP_309421.1	ENSANGP00000011252 [Anopheles ...	32	24	
gi 47222066 emb CAG12092.1	unnamed protein product [Tetrao...	32	24	
gi 23111005 ref NP_002395.1	microfibrillar-associated prot...	32	32	L
gi 5851895 dbj BAA84189.1	techylectin-5B [Tachypleus tride...	32	32	
gi 28868661 ref NP_791280.1	conserved hypothetical protein...	32	32	
gi 38566166 gb AAH62415.1	Microfibrillar-associated protei...	32	32	L
gi 5851897 dbj BAA84190.1	techylectin-5B isoform [Tachyple...	32	32	
gi 27085383 gb AAN85410.1	microfibril-associated glycoprot...	32	32	L
gi 790817 gb AAB00968.1	microfibril-associated glycoprotein 4	32	32	L
gi 21232794 ref NP_638711.1	conserved hypothetical protein...	32	32	
gi 34766451 gb AAQ82564.1	FscC [Streptomyces sp. FR-008]	32	32	
gi 47219763 emb CAG03390.1	unnamed protein product [Tetrao...	32	43	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|31542986|ref|NP_060095.2| **L** intelectin; endothelial lectin HL-1; intestinal receptor [Homo sapiens]
gi|18088358|gb|AAH20664.1| **L** Intelectin [Homo sapiens]
Length = 313

Score = 743 bits (1746), Expect = 0.0

Identities = 263/314 (83%), Positives = 267/314 (85%), Gaps = 32/314 (10%)

Query: 1 M-QLSFLFLIATTRGWSTDEM-TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYPLRT 58
M QLSFLFLIATTRGWSTDE TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLY LRT
Sbjct: 1 MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60

Query: 59 ENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWSSQQGS---WYPEGDGN--M 112
 ENGVYIYQTFCDMTSGGGGWTLVAS EN MRGKCTVGDRWSSQQGS YPEGDGN
 Sbjct: 61 ENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAV-YPEGDGNWAN 119

Query: 113 YNTFGS--MMTSDDY--PGYYDIQ-MDLGIWW-PNKSPMQHWM-SSLLRYRTDTGFLQTL 165
 YNTFGS TSDDY PGYYDIQ DLGIW PNKSPMQHW SSLLRYRTDTGFLQTL
 Sbjct: 120 YNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTL 179

Query: 166 G-ULFGIYQU-PU--GEGKCWTDNGPVIP--NBFGDAQKTASYYSPTYGQREFTAGW-QFR 218
 G LFGIYQ P GEGKCWTDNGPVIP +FGDAQKTASYYSPTYGQREFTAG+ QFR
 Sbjct: 180 GHNLFGIYQKYPVKYGEKGCWTDNGPVIPVVYDFGDAQKTASYYSPTYGQREFTAGFVQFR 239

Query: 219 V--NE-----MCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTN-GYSS 270
 V NE +CAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGT+ GYSS
 Sbjct: 240 VFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSS 299

Query: 271 SREITE-MVLLFYR 283
 SREITE VLLFYR
 Sbjct: 300 SREITEAAVLLFYR 313

☐ >gi|7019846|dbj|BAA90893.1| **L** unnamed protein product [Homo sapiens]
 gi|8096221|dbj|BAA96094.1| **L** intelectin [Homo sapiens]
 gi|18091783|gb|AAL58073.1| **L** endothelial lectin HL-1 [Homo sapiens]
 gi|20377087|gb|AAM20741.1| **L** intestinal lactoferrin receptor [Homo sapiens]
 gi|37181843|gb|AAQ88725.1| **L** ITLN [Homo sapiens]
 gi|37724012|gb|AAO17801.1| **L** intelectin [Homo sapiens]
 gi|44976129|gb|AAS49907.1| **L** omentin [Homo sapiens]
 gi|48146565|emb|CAG33505.1| ITLN1 [Homo sapiens]
 Length = 313

Score = 743 bits (1746), Expect = 0.0
 Identities = 263/314 (83%), Positives = 267/314 (85%), Gaps = 32/314 (10%)

Query: 1 M-QLSFLFLIATTRGWSTDEM-TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYPLRT 58
 M QLSFLFLIATTRGWSTDE TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLY LRT
 Sbjct: 1 MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60

Query: 59 ENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWSSQQGS---WYPEGDGN--M 112
 ENGVYIYQTFCDMTSGGGGWTLVAS EN MRGKCTVGDRWSSQQGS YPEGDGN
 Sbjct: 61 ENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAD-YPEGDGNWAN 119

Query: 113 YNTFGS--MMTSDDY--PGYYDIQ-MDLGIWW-PNKSPMQHWM-SSLLRYRTDTGFLQTL 165
 YNTFGS TSDDY PGYYDIQ DLGIW PNKSPMQHW SSLLRYRTDTGFLQTL
 Sbjct: 120 YNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTL 179

Query: 166 G-ULFGIYQU-PU--GEGKCWTDNGPVIP--NBFGDAQKTASYYSPTYGQREFTAGW-QFR 218
 G LFGIYQ P GEGKCWTDNGPVIP +FGDAQKTASYYSPTYGQREFTAG+ QFR
 Sbjct: 180 GHNLFGIYQKYPVKYGEKGCWTDNGPVIPVVYDFGDAQKTASYYSPTYGQREFTAGFVQFR 239

Query: 219 V--NE-----MCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTN-GYSS 270
 V NE +CAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGT+ GYSS
 Sbjct: 240 VFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSS 299

Query: 271 SREITE-MVLLFYR 283
 SREITE VLLFYR
 Sbjct: 300 SREITEAAVLLFYR 313

☐ >gi|37724005|gb|AA017800.1| ☒ L intelectin [Homo sapiens]
Length = 313

Score = 740 bits (1738), Expect = 0.0

Identities = 262/313 (83%), Positives = 266/313 (84%), Gaps = 32/313 (10%)

Query: 1 M-QLSFLLEFLIATTRGWSTDEM-TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYPLRT 58
M QLSFLLEFLIATTRGWSTDE TYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLY LRT
Sbjct: 1 MNQLSFLLEFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60

Query: 59 ENGVIIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWSSQQGS---WYPEGDGN--M 112
ENGVIIYQTFCDMTSGGGGWTLVAS EN MRGKCTVGDRWSSQQGS YPEGDN
Sbjct: 61 ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKAV-YPEGDNWAN 119

Query: 113 YNTFGS--MMTSDDY--PGYYDIQ-MDLGIWW-PNKSPMQHWM-SSLLRYRTDTGFLQTL 165
YNTFGS TSDDY PGYYDIQ DLGIW PNKSPMQHW SSLLRYRTDTGFLQTL
Sbjct: 120 YNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTL 179

Query: 166 G-ULFGIYQU-PU--GEGKCWTDNGPVIP--NBFGDAQKTASYYSPIYGQREFTAGW-QFR 218
G LFGIYQ P GEGKCWTDNGPVIP +FGDAQKTASYYSPIYGQREFTAG+ QFR
Sbjct: 180 GHNLFGIYQKYPVKYGEKGCWTDNGPVIPVVYDFGDAQKTASYYSPIYGQREFTAGFVQFR 239

Query: 219 V--NE-----MCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTN-GYSS 270
V NE +CAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGT+ GYSS
Sbjct: 240 VFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSS 299

Query: 271 SREITE-MVLLFY 282
SREITE VLLFY
Sbjct: 300 SREITEAAVLLFY 312

☐ >gi|18254480|ref|NP_543154.1| ☒ L intelectin 2; endothelial lectin HL-2 [Homo sapiens]
☐ >gi|18091785|gb|AAL58074.1| ☒ L endothelial lectin HL-2 [Homo sapiens]
☐ >gi|37182928|gb|AAQ89264.1| ☒ L ITLN2 [Homo sapiens]
Length = 325

Score = 534 bits (1252), Expect = e-150

Identities = 217/331 (65%), Positives = 236/331 (71%), Gaps = 66/331 (19%)

Query: 3 LSFLLEFL-IATT-----RGWSTDEMTYFKEWTCSSS-PSLPRSCKEIKDEC 46
L FLLF +AT+ R E F E TC+ S SLPRSCKEIK+ C
Sbjct: 11 LCFLFFSVATSGCSAAAASSLEMLSR-----E---F-E-TCAFSFSSLPRSCKEIKERC 60

Query: 47 PSAFDGLYPLRTENGVIIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWSSQQGS-- 103
SA DGLY LRT+NGV+YQTFCDMTSGGGGWTLVAS EN MRGKCTVGDRWSSQQG+
Sbjct: 61 HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA 120

Query: 104 -WYPEGDGN--MYNTFGS--MMTSDDY--PGYYDIQ-MDLGIWW-PNKSPMQHWM-SSLL 153
YPEGDGN YNTFGS TSDDY PGYYDIQ DLGIW PNKSPMQHW S+LL
Sbjct: 121 D-YPEGDNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALL 179

Query: 154 RYRTDTGFLQTLG-ULFGIYQ-----UPUGEGKCWTDNGPVIP--NBFGDAQKTASY 202
RYRT+TGFLQ LG LFGIYQ GKCW DNGP IP +FGDA+KTASY
Sbjct: 180 RYRTNTGFLQRLGHNLFGIYQKYPVKYRS-----GKCWNDNGPAIPVVYDFGDAKKTASY 234

Query: 203 YSPYGQREFTAGW-QFRV--NE-----MCAGMRVTGCNTEHHCIIGGGGYFPEASPPQCGD 254
 YSPYGQREF AG+ QFRV NE +CAG++VTGCNTEHHCIIGGGG+FP+ P+QCGD
 Sbjct: 235 YSPYGQREFVAGFVQFRVFNNERAAALCAGIKVTGCNTEHHCIIGGGGFFPQGKPRQCGD 294

Query: 255 FSGFDWSGYGTNGYSS-SREITE-MVLLFYR 283
 FS FDW GYGT+ SS SREITE VLLFYR
 Sbjct: 295 FSAFDWDGYGTHVKSSCSREITEAAVLLFYR 325

☐ >gi|6754388|ref|NP_034714.1| **L** intelectin [Mus musculus]
 gi|7513698|pir||JE0328 intelectin - mouse
 gi|3357909|dbj|BAA31992.1| **L** intelectin [Mus musculus]
 gi|12841004|dbj|BAB25043.1| **L** unnamed protein product [Mus musculus]
 gi|37724014|gb|AAO17802.1| **L** intelectin [Mus musculus]
 gi|37724016|gb|AAO17803.1| **L** intelectin [Mus musculus]
 Length = 313

Score = 528 bits (1239), Expect = e-148
 Identities = 213/326 (65%), Positives = 236/326 (72%), Gaps = 56/326 (17%)

Query: 1 M-QLSFLFLIATTRGWSTDEMTYFKEWTCSSS-----PSLPRSCKEIKDE 45
 M QL FLLF++ TRG CS++ SLPRSCKEIK E
 Sbjct: 1 MTQLGFLLFIMVATRG-----CSAAEENLDTNRWGNSFFSSLPRSCKEIKQE 47

Query: 46 CPSAFDGLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWSSQQGSW 104
 A DGLY LRT+NGVIYQTFCDMT+ GGGWTLVAS EN MRGKCTVGDRWSSQQG+
 Sbjct: 48 HTKAQDGLYFLRTKNGVIYQTFCDMTTAGGGWTLVASVHENMRGKCTVGDRWSSQQGNR 107

Query: 105 --YPEGDGN--MYNTFGSM--MTSDDY--PGYYDIQMD-LGIWW-PNKSPMQHW-MSSLL 153
 YPEGDGN YNTFGS TSDDY PGY+DIQ + LGIW PNKSP+ +W SSLL
 Sbjct: 108 ADYPEGDGNWANYNTFGSAEAATSDDYKNPGYFDIQAENLGIWHVPNKSPPLHNWRKSSLL 167

Query: 154 RYRTDTGFLQTLG-ULFGIYQU-PU--GEGKCWTDNGPVIP--NBFGDAQKTASYYSYPYG 207
 RYRT TGFLQ LG LFG+Y+ P GEGKCWTDNGP +P +FGDA+KTASYYSYP G
 Sbjct: 168 RYRTFTGFLQHLGHNLFGLYKKYPVKYGEKGCWTDNGPALPVVYDFGDARKTASYYSYSPG 227

Query: 208 QREFTAGW-QFRV--NE-----MCAGMRVTGCNTEHHCIIGGGGYFPEASPPQCGDFSGFD 259
 QREFTAG+ QFRV NE +CAG+RVTGCNTEHHCIIGGGG+FP+ P QCGDF+ FD
 Sbjct: 228 QREFTAGYVQFRVFNNERAAALCAGVRVTGCNTEHHCIIGGGGFFPEGNPVQCGDFASFD 287

Query: 260 WSGYGT-NGYSSSREITE-MVLLFYR 283
 W GYGT NGYSSSR+ITE VLLFYR
 Sbjct: 288 WDGYGTHNGYSSSRKITEAAVLLFYR 313

☐ >gi|28932914|gb|AAO60215.1| intelectin 2 [Mus musculus]
 Length = 313

Score = 491 bits (1151), Expect = e-137
 Identities = 207/332 (62%), Positives = 230/332 (69%), Gaps = 68/332 (20%)

Query: 1 M-QLSFLLF-LIATTRGWSTDEMTYFKEWTCSSS-----PSLPRSCKEIKD 44
 M QL FLLF +IAT R CS++ SLPRSCKEIK
 Sbjct: 1 MTQLGFLLFIMIAT-R-----VCSAAEENLDTNRWGNSFFSSLPRSCKEIKQ 46

Query: 45 ECPSAFD-----GLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGDRWS 98

E D GLY LRTENGVIYQTFCDMT+ GGGWTLVAS EN +RG+CTVGDRWS
 Sbjct: 47 E-----DTKAQDGLYFLRTENGVIYQTFCDMTTAGGGWTLVASVHENNLGRCTVGDRWS 101
 Query: 99 SQQGSW--YPEGDGN--MYNTFGSM--MTSDDY--PGYYDIQMD-LGIWW-PNKSPMQHW 148
 SQQG+ YPEGDN YNTFGS TSDDY PGY+DIQ + LGIW PN SP+ W
 Sbjct: 102 SQQGNRADYPEGDGNWANYNTFGSAEGATSDDYKNPGYFDIQAENLGIWHVPNNSPLHTW 161
 Query: 149 M-SSLLRYRTDTGFLQTLG-ULFGIYQU-PU--GEGKCWTDNGPVIP--NBFGDAQKTAS 201
 SSLLRYRT TGFLQ LG LFG+YQ P GEGKCWTDNGP P +FGDAQKTAS
 Sbjct: 162 RNSSLLRYRTFTGFLQRLGHNLFGLYQKYPVKYGEKGCWTDNGPAFPVVYDFGDAQKTAS 221
 Query: 202 YYSPYGQREFTAGW-QFRV--NE-----MCAGMRVTGCNTEHHCIGGGGYFPEASPQQCG 253
 YYSP G+ EFTAG+ QFRV NE +CAG+RVTGCNTEHHCIGGGG+FPE P++CG
 Sbjct: 222 YYSPSGRNEFTAGYVQFRVFNNERAASALCAGVRVTGCNTEHHCIGGGGFFPEFDPEECG 281
 Query: 254 DFIGFDWSGYGTN-GYSSSREITE-MVLLFYR 283
 DF+ FD +GYGT+ YS+SREITE VLLFYR
 Sbjct: 282 DFAAFDANGYGTHIRYSNSREITEAAVLLFYR 313

☐ >[gi|45360437|ref|NP_988929.1|](#) ☒ hypothetical protein MGC76330 [*Xenopus tropicalis*]
[gi|38174756|gb|AAH61445.1|](#) ☒ Hypothetical protein MGC76330 [*Xenopus tropicalis*]
 Length = 339

Score = 360 bits (842), Expect = 5e-98
 Identities = 166/288 (57%), Positives = 192/288 (66%), Gaps = 54/288 (18%)

Query: 37 RSCKEIK--DECPSAFDGLYPLRTENGVIYQTFCDMTSGGGWTLVAS-WENRMRGKCTV 93
 RSC EIK D PSA DG+Y L TE+G YQTFCDMT+ GGGWTLVAS EN M GKCTV
 Sbjct: 65 RSCNEIKSSD--PSAPDGIYTLATEHGESYQTFCDMTTNGGGWTLVASVHENNMFGKCTV 122
 Query: 94 GDRWSSQQGSWY----PEGDGN--MYNTFGSM--TSDDY--PGYYDIQ-MDLGIWW- 139
 GDRWS+QQG+ PEGDGN Y TFG + TSDDY PGYYDIQ +L +W
 Sbjct: 123 GDRWSTQQGN--TLQNPEGDGNWANYATFG--LPEGATSDDYKNPGYYDIQAKNLALWHV 178
 Query: 140 PNKSPMQHWM-SSLLRYRTDTGFLQTL--GULFGIYQUPUGE-----GKCWTDNGP 187
 PN +PM +W SS+LRYRT F T G LF +Y GKC DNGP
 Sbjct: 179 PNNTPMFNWRNSSILRYRTQNSFF-TEEGGNLFELY-----KKYPVKYDIGKCLADNGP 231
 Query: 188 VIP--NBFGDAQKTASYSPYGQREFTAGW-QFRV-N-E-----MCAGMRVTGCNTEHHC 237
 +P + G A+KT+S YSP G+ EFTAG+ QFRV N E +C G++V GCN EHHC
 Sbjct: 232 AVPVVYDLGSAEKTSSLYSPNGRNEFTAGFVQFRVVNTEKAALALCPGVKVKGCNAEHHC 291
 Query: 238 IGGGGYFPEASPQQCGDFSGFDWSGYGTN-GYSSSREITE-MVLLFYR 283
 IGGGGYFPE SP+QCGDFS FDW GYGT+ G+S+S+EITE VLL YR
 Sbjct: 292 IGGGGYFPEGSPRQCGDFSADFWDGYGTHAGWSASKEITEAAVLLLYR 339

☐ >[gi|20502359|dbj|BAB91359.1|](#) ☒ 35 kDa serum lectin [*Xenopus laevis*]
 Length = 338

Score = 353 bits (826), Expect = 5e-96
 Identities = 161/286 (56%), Positives = 191/286 (66%), Gaps = 50/286 (17%)

Query: 37 RSCKEIKDECPSAF-----DGLYPLRTENGVIYQTFCDMTSGGGWTLVAS-WENRMRGK 90
 R+C+EIK+ F DG+Y LRT G+ YQTFCDMT+ GGGWTLVAS EN M GK
 Sbjct: 64 RNCREIKE-----FNNNAEDGIYTLRTGGGISYQTFCDMTADGGWTLVASVHENNMFGK 118

Query: 91 CTVGDRWSSQQGS--WYPEGDGN--MYNTFGSMM----TSDDY--PGYYDIQM-DLGIWW 139
 CTVGDRW+SQQG+ YP GDGN Y TFG + TSDDY PGYYDI +LG+W
 Sbjct: 119 CTVGDRWTSQQGNPNYPAGDGNWANYATFG--LPGGATSDDYKNPGYYDITSSNLGLWH 176

Query: 140 -PNKSPMQHWMS-SLLRYRTDTGFLQTL-----GULFGIYQU-PU--GEGKCWTDNGPVI 189
 PN +P HW + SLLRYRT F G LF +YQ P G G C D+GP +
 Sbjct: 177 VPNNTPFShWRNNSLLRYRTQNNF----FSAEGGNLFNLYQKYPLKFGIGTCPKDHGPAV 232

Query: 190 P--NBFGDAQKTASYSPYGQREFTAGW-QFRV-N-E-----MCAGMRVTGCNTEHHCIG 239
 P + G+ T YYSP G+REFTAG+ FRV N E +CAG++VTGCNTEHHCIG
 Sbjct: 233 PIVYDLGNPDLTTKYYSRREFTAGFVHFRVFNAEKAALALCAGVKVTGCNTEHHCIG 292

Query: 240 GGGYFPEASPQQCGDFSGFDWSGYGTN-GYSSSREITE-MVLLFYR 283
 GGGYF E +P+QCGDF+GFDW GYGT+ +S+S+EITE VLLFYR
 Sbjct: 293 GGGYFAEGNPKQCGDFTGFDWDGYGTHQDWSNSKEITEAAVLLFYR 338

☐ >gi|28971732|dbj|BAC65329.1| **L** embryonic epidermal lectin [Xenopus laevis]
 Length = 342

Score = 352 bits (824), Expect = 1e-95
 Identities = 165/289 (57%), Positives = 192/289 (66%), Gaps = 56/289 (19%)

Query: 37 RSCKEIK--DECPS-AFDGLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCT 92
 RSC EIK D S A DG+Y L TE+G YQTFCDMT+ GGGWTLVAS EN M GKCT
 Sbjct: 68 RSCNEIKSSD---SRAPDGIYTLATEDGESYQTFCDMTTNGGGWTLVASVHENNMFGKCT 124

Query: 93 VGDRWSSQQGSWY----PEGDGN--MYNTFGSMM----TSDDY--PGYYDIQ-MDLGIWW 139
 VGDRWS+QQG+ PEGDGN Y TFG + TSDDY PGYYDI+ +L +W
 Sbjct: 125 VGDRWSTQQGN--MLQNPEGDGNWANYATFG--LPEGATSDDYKNPGYYDIEAKNLALWH 180

Query: 140 -PNKSPMQHWM-SSLLRYRTDTGFLQTL--GULFGIYQUPUGE-----GKCWTDNG 186
 PNK+PM W SS+LRYRT GFL T G LF +Y GKC DNG
 Sbjct: 181 VPNKTPMVMWRNSSLRYRTQNGFL-TEEGGNLFELY-----KKYPVKYDIGKCLADNG 233

Query: 187 PVIP--NBFGDAQKTASYSPYGQREFTAGW-QFR-VN-E-----MCAGMRVTGCNTEHH 236
 P +P + G A+KTAS YSP G+ EFT G+ QFR VN E +CAG++V GCN EHH
 Sbjct: 234 PAVPVVYDLGSAEKTASLYSPNGRSEFTPGFVQFRAVNTERATLALCAGVKVKGCNVEHH 293

Query: 237 CIGGGGYFPEASPQQCGDFSGFDWSGYGTN-GYSSSREITE-MVLLFYR 283
 CIGGGGY PEASP+QCGDF+ DW GYGTN G+S+S++I E V+LFYR
 Sbjct: 294 CIGGGGYIPEASPRQCGDFAALDWDGYGTNLGWSASKQIIEAAVMLFYR 342

☐ >gi|20502361|dbj|BAB91360.1| **L** lectin type 2 [Xenopus laevis]
 Length = 315

Score = 338 bits (791), Expect = 2e-91
 Identities = 162/283 (57%), Positives = 184/283 (65%), Gaps = 44/283 (15%)

Query: 37 RSCKEIKDECPSAFDGLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCTVGD 95
 R+CKEIKD SA DG+Y L T NG YQ FCDMT+ GGGWTLVAS EN M GKCTVGD
 Sbjct: 41 RNCKEIKDSDSA KDIYNLITANGETYQAFCDMTTDGGGWTLVASVHENNMFGKCTVGD 100

Query: 96 RWSSQQGSW--YPEGDGN--MYNTFGSMM----TSDDY--PGYYDI-QMDLGIWW-PNKS 143
 RWSSQQG+ P G+GN Y TFG + T DDY PGYYDI DL IW PN +

Sbjct: 101 RWSSQQGNNINNPGGEGNWANYATFG--LPEGATGDDYKNPGYYDISAKDLAIWHVPNNT 158

Query: 144 PMQHWMS-LLRYRTDTGFLQTLG-ULFG-----IYQUPUGEGKCWTDNGPVIP--NB 192
 PM W SS LLRYRT GF + G LF IY G C T+NGP +P +

Sbjct: 159 PMTSWRSSSLLRYRTSNGFFPSEGGNLFNLYKKYPVIYNT----GSCQTNNNGPAVPVLYD 214

Query: 193 FGDAQKTAS-YYSPYQREFTAGW-QFRV-N-E-----MCAGMRVTGCNTEHHCIGGGGY 243
 FGD KT S YYSP G+ EF AG+ QFRV N E +C G++VTGCN EHHCIGGGG+

Sbjct: 215 FGDP-KTTSMYYSPPNGRGEFIAGFVQFRVFENTERAPLALCPGIKVTGCNAEHHCIGGGGF 273

Query: 244 FPEASPQQCGDFSGFDWSGYGTNGY--SSSREITE-MVLLFYR 283
 PE +P QCGDF+ FDW+GYGT GY SS++ ITE VLL YR

Sbjct: 274 IPEGNPVQCGDFAAFDWNNGYGT-GYAWSSTKAITEAAVLLMYR 315

☐ >gi|2632076|emb|CAA57946.1| **L** cortical granule lectin [Xenopus laevis]
 Length = 313

Score = 324 bits (758), Expect = 3e-87
 Identities = 158/284 (55%), Positives = 190/284 (66%), Gaps = 48/284 (16%)

Query: 37 RSCKEIKD---ECPSAFDGLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCT 92
 RSCKEIKD E A DG+Y L + +G+ YQTFCDMT+ GGGWTLVAS EN M GKCT

Sbjct: 39 RSCKEIKDSNEE---AQDGIYTLTSSDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCT 95

Query: 93 VGDRWSSQQGSW--YPEGDGN--MYNTFGSM--MTSDDY--PGYYDIQM-DLGIWW-PNK 142
 +GDRWSSQQG+ YPEGDGN YNTFGS TSDDY PGYYDI+ +LG+W PNK

Sbjct: 96 IGDRWSSQQGNRADYPEGDGNWANYNTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNK 155

Query: 143 SPMQHWMS-SSLLRYRTDTGFLQTL----GULFG---IYQUPU--GEGKCWTDNGPVIP-- 190
 +P+ W SSL RYRT G L G LF IY P G G C D+GP +P

Sbjct: 156 TPLSVWRNSSLQRYRTTDGIL---FKHGGNLFSLYRIY--PVKYGIGSCSKDSGPTVPVV 210

Query: 191 NBFQDAQKTASYSP-YGQR-EFTAGW-QFR-VN-E-----MCAGMRVTGCNTEHHCIGG 240
 + G A+ TAS+YSP + R +FT G+ QFR +N E +C GM++ CN EH CIGG

Sbjct: 211 YDLGSAKLTASFYSPDF--RSQFTPGYIQFRPINTEKAALALCPGMKMESCNVEHVCIGG 268

Query: 241 GGYFPEASPQQCGDFSGFDWSGYGTNGYSSS-REITE-MVLLFY 282
 GGYFPEA P+QCGDF+ +D++GYGT ++S+ EITE VLLFY

Sbjct: 269 GGYFPEADPRQCGDFAAYDFNGYGTKKFNSAGIEITEAAVLLFY 312

☐ >gi|1841845|gb|AAB47537.1| **L** lectin [Xenopus laevis]
 Length = 313

Score = 322 bits (753), Expect = 1e-86
 Identities = 158/283 (55%), Positives = 189/283 (66%), Gaps = 46/283 (16%)

Query: 37 RSCKEIKD---ECPSAFDGLYPLRTENGVIYQTFCDMTSGGGGWTLVAS-WENRMRGKCT 92
 R+CKEIKD E A DG+Y L + +G+ YQTFCDMT+ GGGWTLVAS EN M GKCT

Sbjct: 39 RNCKEIKDSNEE---AQDGIYTLTSPDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCT 95

Query: 93 VGDRWSSQQGSW--YPEGDGN--MYNTFGSM--MTSDDY--PGYYDIQM-DLGIWW-PNK 142
 +GDRWSSQQG+ YPEGDGN YNTFGS TSDDY PGYYDI+ +LG+W PNK

Sbjct: 96 IGDRWSSQQGNRADYPEGDGNWANYNTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNK 155

Query: 143 SPMQHWMS-SSLLRYRTDTGFLQTL----GULFG---IYQUPU--GEGKCWTDNGPVIP-- 190